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AMENDMENTS

In the Specification

Please amend the paragraph beginning on line 28 in the specification to read as follows:

Kyte-Doolittle hydrophilicity analysis suggested twelve hydrophobic stretches suitable for formation of TMDs that are well aligned with similar profiles of transporters in the *gat*1/ *net* gene family. Two canonical sites for N-linked glycosylation are located in the large hydrophilic loop between TMDs 3 and 4, sites analogous to those known to be glycosylated in mammalian catecholamine transporters (Melikian *et al.*, 1996). Additional N-glycosylation sites are present in the transporter's amino (N22) and carboxyl (N597) termini. The amino and carboxyl termini possess a number of Ser and Thr residues that may be targets for regulatory phosphorylation with two PKC sites (Ser45, Ser582) and one casein kinase II site (Thr580). A cAMP-dependent protein kinase site (Ser255) also lies in a putative intracellular loop between tmdsTMDs 4 and 5 within a span of residues (WKGXXTSGKVVW) (SEQ ID NO: 3) found in all catecholamine transporters. Similarly, a casein kinase II site between TMDs 6 and 7 lies in a highly conserved stretch of sequence (A(Y/F)SSYN(D/K)F (SEQ ID NO: 4). Comparisons with other *gat*1/*net* family members demonstrates highest similarity of CeDAT to mammalian catecholamine transporters. CeDAT exhibits 47% amino acid identity with human, mouse, and bovine NETs, 43% identity with human, bovine, and rat DATs, 37% identity with human, rat and, mouse SERTs, and less than 35% identity with other gene family members. Sequence divergence suggests the carrier may have arisen from a common ancestral transporter before DATs, NETs, and ETS formed genetically distinct species. An Asp residue that is conserved in TMD1 of the DA, NE and 5HT transporters from fly to man (Kitayama *et al.*, 1992; Barker and Blakely, 1995)

but absent from GABA, glycine, taurine, proline, creatine and taurine transporters, is also present in an analogous position (D60) in CeDAT. Thus, there is sequence divergence and conservation that is evident comparing CeDAT with its most closely related mammalian homologs.